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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/963,790	09/27/2001	Mike Farwick	32301WD230	9133

7590 04/10/2007
SMITH, GAMBRELL & RUSSELL, LLP
SUITE 800
1850 M STREET, N.W.
WASHINGTON, DC 20036

EXAMINER

STEADMAN, DAVID J

ART UNIT	PAPER NUMBER
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1656

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	04/10/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

DETAILED ACTION

Status of the Application

[1] Claims 5, 9, 12, 34-35, 37-38, 40, 42, 44, 46, 48, and 51-56 are pending in the application.

[2] Applicant's amendment to the claims after final rejection, filed on 3/12/07, is acknowledged and has been entered into the application. This listing of the claims replaces all prior versions and listings of the claims in accordance with 37 CFR 1.121(c).

[3] Applicant's arguments filed on 3/12/07 in response to the Office action mailed on 12/11/06 have been fully considered and are deemed to be persuasive to overcome some of the rejections and/or objections previously applied. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

[4] The text of those sections of Title 35 U.S. Code not included in the instant action can be found in a prior Office action.

Claim Rejections - 35 USC § 112, Second Paragraph

[5] Claim(s) 55-56 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 55 (claim 56 dependent therefrom) is drawn to a method for producing L-amino acids by cultivating the recited host cell and attenuating expression of the recited nucleic acids. However, the claim does not require that the recited host cells comprise

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the recited *isolated* nucleic acids. As such, it is unclear as to whether or not the recited host cell comprises the recited *isolated* nucleic acids. It is suggested that applicant clarify the meaning of the claim.

Claim Rejections - 35 USC § 112, First Paragraph

[6] Claims 55-56 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a new matter rejection.

MPEP § 2163 states, "when filing an amendment an applicant should show support in the original disclosure for new or amended claims" and "[i]f the originally filed disclosure does not provide support for each claim limitation, or if an element which applicant describes as essential or critical is not claimed, a new or amended claim must be rejected under 35 U.S.C. 112, para. 1, as lacking adequate written description."

Claim 55 (claim 56 dependent therefrom) is drawn to (in relevant part) a method for the fermentative preparation of L-amino acids comprising the step of cultivating a recombinant *Escherichia coli* host cell. While the specification would appear to support an *Escherichia coli* host cell transformed with a vector comprising the recited nucleic acids (see, e.g., paragraphs 29, 31, 62, 64, 85, and original claim 12). However, the examiner can find no support in the original application for the concept of using an *Escherichia coli* host cell for L-amino acid production.

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Also, the method of claim 55 does not appear to be supported by the original disclosure. Examples 4 and 5 (beginning at p. 27 of the specification) provide support for a method for producing L-amino acids by culturing a *C. glutamicum* host cell, which has an attenuated endogenous *deaD* gene, wherein the gene is attenuated prior to culturing of the host cell. However, the method of claim 55 (claim 56 dependent therefrom) involves culturing of the recited host cell *followed by* attenuation of expression of an *isolated* nucleic acid, including fragments of SEQ ID NO:1. Because the recited nucleic acid of the host cell is *isolated*, this suggests that the host cell is transformed with the recited nucleic acid and then expression of the isolated nucleic acid is subsequently attenuated. Further, the claimed method encompasses attenuation of expression of fragments of SEQ ID NO:1. In this case, the original application does not appear to provide support for such a method. Applicant is invited to show support for claim 55 in the original application.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

[7] The indicated allowability of claims 40, 42, 46, and 48 is withdrawn in view of the newly discovered reference(s) to Pompejus et al. (US Patent Application Publication

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2006/0269975). A rejection based on the newly cited reference follows. It is noted that this reference was only made publicly available after the sequence search conducted on 6/2/2006.

[8] Claim(s) 40, 42, 46, and 48 are rejected under 35 U.S.C. 103(a) as being unpatentable over Pompejus et al. (US Patent Application Publication 2006/0269975), which claims priority under 35 U.S.C. 119(e) to US provisional application 60/144,448, filed on 7/16/99. The claims are drawn to an isolated polynucleotide consisting of a fragment of SEQ ID NO:1 or its complement, wherein the fragment consists of at least 30 or 40 consecutive nucleotides.

Pompejus et al. teaches a nucleic acid, SEQ ID NO:143, which comprises SEQ ID NO:1 herein with the exception of two mismatches at positions 273 and 479 of SEQ ID NO:1 (Appendix A). Pompejus et al. teaches oligonucleotide primers that are at least 40 consecutive nucleotides of SEQ ID NO:143 (p. 11, paragraph 73) for use in amplifying coding sequence and 3'-untranslated sequence downstream of SEQ ID NO:143 (p. 10, paragraphs 66-67 and p. 11, paragraph 73). Although Pompejus et al. suggests fragments of SEQ ID NO:143 that would be encompassed by claims 40, 42, 46, and 48 herein, the reference of Pompejus et al. does not specifically teach a polynucleotide consisting of at least 30 or 40 consecutive nucleotides of SEQ ID NO:1 herein.

It would have been obvious to one of ordinary skill in the art to make: 1) an antisense PCR primer that is at least 30 or 40 consecutive nucleotides and is complementary to the 3'-end of SEQ ID NO:1 with the primer's 5'-nucleotide being at

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nucleotide 2130 of SEQ ID NO:1 herein and 2) a sense PCR primer that is at least 30 or 40 consecutive nucleotides and is identical to the 3'-end of SEQ ID NO:1 with the primer's 3'-nucleotide being at nucleotide 2130 of SEQ ID NO:1 herein (see diagram at p. 2 of Appendix A). One would have been motivated for an antisense PCR primer that is at least 30 or 40 consecutive nucleotides and is complementary to the 3'-end of SEQ ID NO:1 with the primer's 5'-nucleotide being at nucleotide 2130 of SEQ ID NO:1 herein in order to PCR amplify SEQ ID NO:143 as suggested by Pompejus et al. One would have been motivated to make a sense PCR primer that is at least 30 or 40 consecutive nucleotides and is identical to the 3'-end of SEQ ID NO:1 with the primer's 3'-nucleotide being at nucleotide 2130 of SEQ ID NO:1 herein in order to PCR amplify 3'-untranslated sequence downstream of SEQ ID NO:143 as suggested by Pompejus et al. One would have a reasonable expectation of success for making the primers noted above because of the results of Pompejus et al. Therefore, claims 40, 42, 46, and 48, drawn to nucleic acid fragments of SEQ ID NO:1 as noted above, would have been obvious to one of ordinary skill in the art at the time of the invention.

In order to clarify the record, it is noted the sequence of SEQ ID NO:143 of Pompejus et al. was first disclosed in US provisional application 60/144,448, filed on 7/16/99 (see Appendix B).

Conclusion

[9] Status of the claims:

Claims 5, 9, 12, 34-35, 37-38, 40, 42, 44, 46, 48, and 51-56 are pending.

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Claims 5, 9, 12, 34-35, 37-38, 44, and 51-54 appear to be in a condition for allowance.

Claims 40, 42, 46, 48, and 55-56 are rejected.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David J. Steadman whose telephone number is 571-272-0942. The examiner can normally be reached on Mon to Fri, 7:30 am to 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr Bragdon can be reached on 571-272-0931. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file us-09-963-790a-1.res made by tport on Tue 27 Mar 107 15:02:26-PDT.

Query sequence being compared: US-09-963-790A-1 (1-2381)
Number of sequences compared: 513

Number of sequences searched:

Number of scores above cutoff:

Results of the initial comparison of US-09-963-790A-1 (1-2381) with
File : US11370121.seg

	1000-	500-	100-	50-	10-
N	-	-	-	-	-
U	-	-	-	-	-
M	-	-	-	-	-
B	-	-	-	-	-
E	-	-	-	-	-
R	-	-	-	-	-
O	-	-	-	-	-
F	-	-	-	-	-
S	-	-	-	-	-
E	-	-	-	-	-
Q	-	-	-	-	-
U	-	-	-	-	-
E	-	-	-	-	-
N	-	-	-	-	-
C	-	-	-	-	-
E	-	-	-	-	-
S	-	-	-	-	-

5.

SCORE	STDEV
0	0
1	239
2	478
3	717
4	956
5	1195
6	1434
7	1673
8	1912
9	2151

PARAMETERS

	Unary	K-tuple
Similarity matrix	1	4
Mismatch penalty	1	30
Gap penalty	5.00	Joining penalty
Gap size penalty	0.33	Window size
Scaloff score	1	500
Randomization group	0	

SEARCH STATISTICS

Mean	Median	Standard Deviation
74	58	146.44

Times:	CPU	Total Elapsed
	00:00:00.02	00:00:00.00

Number of residues:	245221
Number of sequences searched:	217
Number of scores above cutoff:	217

A 100% identical sequence to the query sequence was not found. The scores below are sorted by initial score. Significance is calculated based on initial score.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame

1. US-11-370-121-14 Sequence 143, Application 2319 2151 2151 14.18 0

1. US-09-963-790A-1 (1-2381)
US-11-370-121-14 Sequence 143, Application US/11370121

```
Initial Score = 2151 Optimized Score = 2151 Significance = 14.18
Residue Identity = 99% Matches = 2151 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0
```

120
 130
 140
 150
 160
 170
 180

ACCTCAACGGGACGTGAAACAGCCCAATTAAGTCATTTCGCGAATCTCAGAAACCCCGACGGTACT

X
 10
 20
 CAGAAACCCCGACGGTACT

30 40 50 60 70 80 90
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CAGCATCAGCTGACTTGGCTTGCAGAACCCCAACCAACACTGTTGAAGATGACCGACGACTTGTAGGGTATGCC
190 200 210 220 230 240 250 260

100 110 120 130 140 150 160
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170 180 190 200 210 220 230
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340 350 360 370 380 390 400
TCAATGGAATGAGACTCTTCGGAGGTGTCAACAGCCTTCAACAGCATCTCTTACGGAAGCCAAAT

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410 420 430 440 450 460 470
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CCCAATTAGGCAAAACCATCCCAATCTCATGAGGGCAGAGTGTGTTGTTAGACAGACCGTA
320 330 340 350 360 370 380
CCCAATTAGGCAAAACCATCCCAATCTCATGAGGGCAGAGTGTGTTGTTAGACAGACCGTA
480 490 500 510 520 530 540

390 400 410 420 430 440 450
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CCGGTAAGACTGCAAGCTTTGGCGCGTCGCAATCTTTCGCCGATTGCAAGTCCGCGCCAGCCCAAGGAC
550 560 570 580 590 600 610 620
CCGGTAAGACTGCAAGCTTTGGCGCGTCGCAATCTTTCGCCGATTGCAAGTCCGCGCCAGCCCAAGGAC

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530 540 550 560 570 580 590

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600 610 620 630 640 650 660 670
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800 810 820 830 840 850 860 870 880 890 900
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750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900
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820 830 840 850 860 870 880 890 900
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960 970 980 990 1000 1010 1020 1030 1040 1050
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1110 1120 1130 1140 1150 1160 1170 1180 1190
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GCCGCTGTGTGACAGAGCTTACGGCATTCAGCTCTGTGCGTGTGGCG
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|
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1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410
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|
|
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1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480
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|
|
|
CACCAGTGTGTGACAGAGCTTACGGCATTCAGCTCTGTGCGTGTGGCG
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1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550
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Coding Sequence

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|
|
|
ACGAGTGTGTGACAGAGCTTACGGCATTCAGCTCTGTGCGTGTGGCG
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1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
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1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
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1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910
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1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990
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|
|
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2000 2010 2020 2030 2040 2050 2060
1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060
ACTCGGTGTGTGACAGAGCTTACGGCATTCAGCTCTGTGCGTGTGGCG
|
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1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130
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2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270
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2280 2290 2300 2310
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Untranslated Sequence

~~APPENDIX A~~: DNA SEQUENCES

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>RXA00045
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>RXA00050-upstream
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>RXA00050
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GATACTTCTGAGGACGCCGACTCTGCAGATGCAGACAACGCGAGCAATGTAATCAATGAG
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GGTTACGAAACTCCTTCCCAATTACAGGCACAAACCATCCCAATCCTCATGGAGGGCCAG
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CTTGCCCGTATTGACAAGTCCGTGCGCAGCCACAGGCACTTGTGCTTGCCCTACCCGT
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GACACCGAGTCCTACGTTACCCGCATCGGCCGACCCGGCCGTGCAGGACGTACCCGGCGAG
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AACGCACCACTGCACGAAATGGAAGTGGCAACCGTCGATCAGGTCAACGACTTCCGCAAG
GTCAAGTTCGCTGACTCCATCACCAAGTCCCTCGAGGACAAGCAGATGGACCTGTTCCGC
ACCCTGGTCAAGGAATACTCCAGGCCAACGACGTTCTCTAGAGGACATCGCAGCGGCA
CTGGCAACCCAGGCACAGTCCGGCGACTTCTGCTCAAGGAGCTCCACCCAGAGCGCGGT
GAGCGCAACGACCGCCGTCGTGACCGTGACTTCGACGACCGTGGTGGACGTGGACGCGAC
CGTGACCGTGGCGACCGCGGAGATCGTGCTCACGCTTCGACCGCGACGACGAGAACCTG

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GCACCTTGCCAACGAAGGTGGCCTGAACTCCAAGGACTTCGGCCGCATCACCATCGCAGCC
GACCACACCCTGGTTGAACTGCCAAAGGATCTCCACAGAGCGTTCTTGACAACCTGCGC
GACACCCGCATCTCCGGCCAGCTCATCAACATAGAACGCGACTCCGGTGGACGCCACCA
CGCCGCTTCGAGCGCGATGACCGTGGCGGACGCGCGGATTCCGCGGCGACCGTGATGAC
CGCGGTGGACGTGGACGTGACCGTGACGATCGTGGAAGCCGTGGAGGTTTCCGCGGTGGA
CGTGACCGTGATGATCGTGGCGGACGCGGTGGATTCCGCGGACGCGACGACCGCGGAGAC
CGTGGTGGCCGTGGCGGTTACCGTGGCGGACGCGAC

>RXA00050-downstream
TAAGAGTTCGTTTTAGCTTCAGC

>RXA00157
GCCCGCATCGTTGCTGAGCAGCGTGAGGCGGAAGCCGTGAAAAGAAAGTCCAGACCCAG
GCTGCAATTGCCGCAAACAGCGAGCAGCTCAATGTCTTGACTACCAATCGCAGTACCTTG
GTTGCCAGCGTGATGGGGCTGAGCGCAACTTGGCCATCGCTCGTGCGCAGGCGGATAAT
CTGCAAGGTGAGCGTGCTGAGTACGAGGAATTCCAGCAGGCAGAGCAGGCTCGCATCCAG
GCGGAAGCGGAAGCTCAGGCTGCTGCGGAGGAGAAGCGTCGTGCCGATGAGGCTGCTGCA
CAGGCAGCGCTGAAGCTCAAGAAGCTGCCCAGCAAGCTCAGGCGGCGGAGGAAGCCCAA
GCCGCGCAACAGCTGAGACAGCACAAGCCCAAGCCGCGCAAGCTGCGGAAACCCAAAGCT
GCACAAGCCGCGCAAGCTCAGGCAGAAGCGAATGATCGTGCCGCGCGCAACAGCGTGCT
GCAGAGGCTCAAGCAGCAGCGGAACAGGCGCAACGTGAGGCTGAAGCTCAGGCGGCCAAC
GATGCCCAAGCTCAGGCAGTGCCTGAACAGGCGCTCACCAGCAGCTCCATCGCTGCGGCT
GCTCTAATTGCGGCGAGCCAGTCCAGCCATGCCACTACTCATAATCCTTACCCAACTGAT
GAAGACGCGGATCCGACCGATATTGCGGACATCCAAGGCCCAACGCAGCCAGGTACGGGT
GAGTCTGGAGATTCCCAAGCAACTCCAGCGACAACGATTCCACAGGCAACGATTCCACA
GGCTCTGACTCTTCAGATTGAGATTCCCTCCGGCAACGATTCTTCAGAGGTTATTTCCGGC
GATCGTTCCGCTCAGATTGAGACTGTGATTGCGCGCGCCATGAGCCAGTTGGGTGTGCAG
TACGCATGGGGTGGCGGTAACGCTAATGGCCCAACTCTGGGTATCCGTGACGGTGGCGTG
GCGGACTCTTACGGCGATTACAACAAGGTTGGCTTCGACTGCTCTGGACTGACCTTGTAT
CGTTTGGCGGTGTGGGAATTTCACTTCTCACTACACGGGCTACCAGTACCAGCACGGC
ACCAAGGTGTGCGCTTCTGAGATGCAACGTGCGCATCTGATCTTCTATGGTCCGGGAGCG
TCTCAGCACGTGGCAATTTACCTCGGTGATGGTCAGATGATTGAGGCTCCGAATTCGGGT
TCTGTCGTGAAGATTCTCCTGTTGCTGAGCGGAATGACCGAGAGCGTGGTACGCCTC
ATT

>RXA00157-downstream
TAGTTTCCTCCTATGAATCTTGA

>RXA00060-upstream
TGAAAGCAATATTAGACCATCAATGATTAGGAATGGAATTAGGGGTCTGGTTTGGGTGA
ATGTGTCGCTAATTTTTTCCACTCGCCTACACTCGGGAGGC

>RXA00060
GTGACTGAGAAGACTGACAGACCTTAATGCTTATCGACGGCCACTCGATGGCTTTCCGC
GCATTCTTTGCTTTGCCGGCTGAGAATTTCTCCACGTCCGGCGGGCAGGCCACCAATGCT
GTCTATGGCTTTCTCTCGATGCTGTCCACGTTGTTGAAGGATGAGCAGCTACTCATGTG
GCGGTGGCTTTGATGTGGGGCGTAAGACGTTCCGTACCGATATGTTCCGGCGGTATAAG
GCGCAGCGTGAAGCAACGCCACCTGAGTTTAAGGGCCAGGTGGAATCCTCAAGGAGGTG
TTGTCCACTTTGGAATTACGACTATTGAGAAAATCGATTTTGAGGCTGATGATGTGATC
GCCACGTTGTCTGTGGCGGCGAAACCTTTAGGCTTTAAGACGCTGATTGTTACGGTGAC
CGTGATTCTTCCAGTTGGTCAATGACACCACCGGTGTTGTATCCGATGAAGCGCGTG
TCTGTGCTGCACCGTTTACGCCGGAAGCAGTGAGGAGAAGTATGGACTGACACCGAGG
CAGTATCCGGAGTTTGCAGCGCTGCGTGGTGATCCTTCCGATAACTTGCCTAATATTCCT
GGCGTGGCGGAGAAGACTGCTACCAAGTGGATTGCCAGTATGAACTTTGGATAATTTG
CTTGATCACGCTGATGAGATCAAGGGCAAGGTTGGCGCCAGCCTGCGTGAGCGCATTGAG
CAGGTCCGGATGAACCGCAAGCTCACGGAGATGGTGAAGGATCTGGAGCTGCCGCTTGGT
CCGACGATTTTGAAGATGAAGCCTGTGCAGGTTGCGGAGGTTGCGGCGAAGTTGACGAT
CTGGAGTTTGGTACCAATTTGCGTGAGCGGCTGCTGGCGGTGGTGAAGGCCGAGGGTTCC
GCTGCCCCCGTGGAGGAAGTGAAGCGGAACAGGTTGTCGTCGATACGAATCTTTGGCG
CAATGGCTGCCTGCTAGGGCTGGCCAGGCGCTTGCTTTAGCGCTGGCTGGAGTGGCTAAA

~~APPENDIX B: AMINO ACID SEQUENCES~~JCS49 U.S. PRO
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~~1-909, translated) 303 residues~~
~~CTCTLAL DIGATKIAYA LVPDNTPTTT LSTGRLGTKE GDSPIEQIRE VLLAGLKAAE~~
~~EHGLSVARIG MGAPGVILGP EGTIVYNGET LTFWACTDLR GLSREVLNVP FAAHNDVRVW~~
~~AYGEHHLGTG KDLTGRLVLYV SLGTGVGGAI IEDGIMMSSP TGTAGEFAEV VCS DHAGLAV~~
~~RCENVASGTG LTRYYNAAAA TQLDLPAIME RFHQGDGLAO QIITGNLRGF GOALGALVTV~~
~~LDLSAVVVGG GVAGIGAPVM DPITAGIFDR VLTPNKSQVQ LSTSLGAQAA VIAAAKYARD~~
~~NAF~~

> RXA00050 (1-2196, translated) 732 residues
 MSNTENVNGD VEQPNNVISS ESQETPOGDS ASADFALETP TNTVEDAPAS EGSEEITRVA
 DTSEDADSAD ADNASNINE NEDSSEGANQ PSNESSSTEAS KSGFDALGLP ERVLDAVRKV
 GYETPSPIQA QTIPILMEGQ DVVGLAQTGT GKTAALFALPI LARIDKSVRS PQALVLAPTR
 ELALQVADSF QSFADHVGGI NVLPIYGGQA YGIQLSGLRR GAHIVVGTGP RIIDHLEKGS
 LDISGLRFLV LDEADEMLNM GFQEDVERIL EDTPDEKQVA LFSATMPNGI RRLSKQYLNN
 PAEITVKSET RTNTNITQRF LNVHRNKMD ALTRILEVTE FEAMIMFVRT KHETEEVAEK
 LRARGFSAAA INGDIQAQOR ERTVDQLKDG RLDILVATDV AARGLDVERI SHVLNFDIPN
 DTESYVHRIG RTGRAGRTGE AILFVTPRER RMLRSIERAT NAPLHEMELP TVDQVNDFRK
 VKFADSITKS LEDKQMDLFR TLVKEYSQAN DVPLEDIAAA LATQAQSGDF LLKELPPERR
 ERNDRRRDRD FDDRGGGRGD RDRGDRGDRG SRFRDDENL ATYRLAVGKR QHIRPGAIVG
 ALANEGGLNS KDFGRITIAA DHTLVLPKD LPQSVLDNLR DTRISGQLIN IERDSGGRPP
 RRFERDDRGG RGGFRGDRDD RGGGRDRDD RGSRGGRGG RDRDDRGGRG GFRGRDDRGD
 RGGRGGRGG RD

> RXA00060 (1-2457, translated) 819 residues
 VTEKTDQTLN LIDGHSMAFR AFFALPAENF STSGGQATNA VYGFLSMLST LLKDEQPTHV
 AVAFDVGRKT FRDMPFAYK AQREATPPEF KGQVEILKEV LSTLGITTE KIDFEADDVI
 ATLSVAAKPL GKTLIVTGD RDSFQLVNDT TTVLYPMKGV SVLHRTPEA VEEKYGLTPR
 QYPEFAALRG DPSDNLNIP GVGEKTATKW IAQYETLDNL LDHADEIKGK VGASLRERIE
 QVRMNRKLT MVKDLELPLG PDDFEMKPVQ VAEVAAKFDD LEFGTNLRER VLAVVKAEGS
 AAPVEEVEAE QVVVDTSLSA QWLPARAGQA LALALAGVAK PAAGDTYALA IAADYKRAVL
 VDVADISAED EKALATWLAS EDPKMLHCAK AAYHMLAGRG FELHGVVHDT AIAATYLLRPG
 QRTYELADVY QRHLQRLST NDNCGQLTLL DAADDQSIVD DVIAILELSE ELTKQLQEIQ
 AFELYHDLEI PLSGILARME AIGIAVDVAT DEEQLKTFIG QVAQEEEEAR ELAEDPTLNL
 SSPKQLQVVL FETFGMPKTK KTKTGYSTAA AEIBALAIKN PHPFLDHLLA HRQYQKMKTT
 LEGLIREVAP DGRHTTFNQ TVASTGRLLS TDPNLQNTPV RTEAGRKIRS GFVVGEGET
 LLTADYSQIE MRVMAHLSQD PGLIEAYREG EDLHNYVGSK VFNVPIDGVT PELRRQVKAM
 SYGLVYGLSA FGLSQQLSIP AGEAKQIMES YFERFEGVQR YLREIVEEAR KAGYTETLFG
 RRRYLPELTS DNRVARENAE RAALNAPIRE LPQTSSRWP

> RXA00061 (1-210, translated) 70 residues
 MIRVDRSLKE AAVKSRVLLQ VHDELVEVA AGELEQVREI LEREMDNAIK LSVPLEVSAG
 DGVNWDAAAH

> RXA00066 (1-813, translated) 271 residues
 VTDPLSALD SGRINHAYLF SGPRGCGKTS SARILARSLN CVEGFTSTPC GVCNSCVALA
 PGGPGTLDVT ELDAASNNGV DDMRELREAR NYAPAESRYR VTIIDEAHMI STQGFNALLK
 IVEEPPAHLI FIFATTEPDK MGTIRSRTH NYPFRLLTPG DMRKVLKNAV DGEVHVDDSD
 VYPLVIRAGG GSPRDSLSIL DQLIAGSGPE GLTYERLPL LGVTSFTLID DSIHALASKD
 NASMFTTIDN VIEEGLEPRR FTIDLPSDEL R

> RXA00095 (1-2289, translated) 763 residues
 MNTSPFTPGS PDLIDGLNEQ QRAAVEHIGS PLLIVAGAGS GKTAVLTRRI AYLMYRGRVH
 PQQILAITFT NKAAMEMPER VSQLVGPVAE RMWVATFHSV CVRILRQQAQ LVEGLNTNFT
 IYDSDDSRRL LTMIAKDLEL DIKKFSARTL LGAISNLKNE LVTPQEALAD AERTHNPYET
 VVARAFSEYQ SRLRRANAVD FDDLIGETVR IFREHPPVAE YYRRFRHVL IDEYQDTNHA
 QYELISTLYG KPDQDPSELG VVGDSQSIY AFRGATIRNI EEFERDESNA RTILLEQNYR
 STQTILSAAN AVISQENRR PKNLWTALGE GEQIGYVAD NEHDEARFIA SEIDNLVDHG
 MSYSDIAIMY RTNNSRRALD DVMRTGVPI KVVGGTKFYE RKEIRDIIAY LRVLENPDDT
 VNLRRRIINTP KRGIGDRAQA FIALHSENNQ ISFGQALLDA ALGKVDLLGA RGKNAAIKFN